

Application No.: 10/718952
Docket No.: BB1077USDIV

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REMARKS

Claims 1,3,4,6,7,9 and 10 are currently pending in the application.

Claims 1 and 7 have been amended and the term "using" has been replaced with the term "based on". Support for this change is found throughout the specification as filed, for example on page 10 at lines 17-31. It is believed that no new matter has been added.

The text added to claim 7 "or 11 based on the Clustal method of alignment" has been underlined and is now in compliance with Rule 1.121 which requires that the text of any added subject matter to be shown by underlining. No new matter has been added.

Claim 4 has been amended for purposes of clarification. It is believed that no new matter has been added.

Claims 1 and 7 were rejected under 35 U.S.C. § 112 , first paragraph, as being indefinite for failing to particular point out and distinctly claim the subject matter which applicant regards as the invention. The term "the Clustal method of alignment" refers to the Clustal method of alignment described in the specification on page 10 at lines 24-30. Withdrawal of this ground of rejection of claims 1 and 7 is respectfully requested in view of the above discussion and amendments.

Claims 1 and 6-7 were rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the enablement requirement, on the ground that the specification does not reasonably provide enablement for all nucleic acid fragments encoding a soybean myo-inositol phosphate synthase (MIPS) including those that have 90% sequence identity to SEQ ID NO: 1,5,11 or 15 and the complement or subfragment thereof.

Enclosed herewith is Appendix A sets forth a comparison of the nucleic acid sequences of wild type and mutant soybean *myo*-inositol 1-phosphate synthases.

This alignment also identifies the conserved nucleic acid sequence motifs corresponding to the amino acid sequence motifs disclosed by Majumder et al. (2003, FEBS Lett. 553: 3-10) and Majumder et al (1997, Biochim. Biophys. Acta 1348: 245-256):

a) the GXGGXG motif is set forth as GWGGNNG in the sequences of the invention and corresponds to the underlined nucleic acid sequence designated Motif I;

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- b) the "LWTANTERY" motif corresponds to the underlined nucleic acid sequence designated Motif II;
- c) the "NGSPQNTFVPGL" motif corresponds to the underlined nucleic acid sequence designated Motif III; and
- d) the "SYNHLGNNDG" motif corresponds to the underlined nucleic acid sequence designated Motif IV.

All of these motifs are conserved at the nucleic acid level among the sequences of the invention. Altogether, 114 nucleic acid residues are encompassed.

Furthermore, the instant specification also discloses the following:

- a) two allelic wild-type soybean MIPS nucleic acid sequences (SEQ ID NO: 1 and 15 that vary in 42 nucleic acid residues as indicated by an open arrow in the alignment set forth in Appendix A. Since SEQ ID NOs 1 and 15 correspond to wild type MIPS, it appears that these variations in the nucleic acid sequence do not affect functionality of the enzyme; and
- b) two mutant soybean MIPS nucleic sequences as set forth in SEQ ID NOs: 5 and 11 that have 2 nucleotide changes. These changes are indicated by a darkened triangle appearing over the mutated residues. These mutated residues appear to be important for functionality of the enzyme.

Thus, 158 nucleic acid residues, out of the approximately 1500 coding for a soybean MIPS, have been described in terms of importance to maintain or alter function of a MIPS enzyme. Therefore, it is believed that sufficient guidance has been provided to one of ordinary skill in the art as to which soybean nucleic acid fragments within 90% sequence identity, subfragments and complements thereof constitute a part of the invention. One of ordinary skill in the art would be able to practice the instant invention without engaging in undue experimentation to screen through a vast number of soybean clones to identify those having 90% sequence identity with the claimed sequences encoding either a wild type MIPS or a mutant MIPS.

Accordingly, withdrawal of the rejection of the claims under 35 U.S.C. § 112, first paragraph, as lacking enablement is respectfully requested.

A petition for an Extension of Time for One (1) month accompanies this response along with Appendix A and a Notice of Appeal.

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It is respectfully submitted that the claims are now in form for allowance which allowance is respectfully requested.

Please credit any overpayment and charge any fees which are required in connection with the filing of the response to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Respectfully submitted,

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Dated: August 15, 2006

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APPENDIX A

Appendix A shows a comparison of the nucleic acid sequences of wild type and mutant soybean *myo*-inositol 1-phosphate synthases. Dashes are used by the program to maximize alignment of the sequences. The conserved nucleic acid sequences (motifs I, II, III and IV) corresponding to the amino acid sequence motifs disclosed by Majumder et al. (2003, FEBS Lett. 553: 3-10) and Majumder et al (1997, Biochim. Biophys. Acta 1348: 245-256) are underlined. Forty-two nucleic acid residue changes in the two allelic wild-type soybean *myo*-inositol 1-phosphate synthases (SEQ ID NO: 1 and 15) are indicated by an open triangle above the alignment. Nucleic acid residue changes in the nucleic acid sequences of mutant lines corresponding to SEQ ID NO: 5 and 11 are indicated by a closed or darkened triangle above the alignment.

SEQ ID NO:1	CTCTTCTTTATCCTTTGTAATTCAATTCAATTCTTAATCTTGTAAGAAATAATGTTCA
SEQ ID NO:5	----- ATGTTCA
SEQ ID NO:9	----- ATGTTCA
SEQ ID NO:11	----- ATGTTCA
SEQ ID NO:13	----- ATGTTCA
SEQ ID NO:15	----- ATGTTCA
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SEQ ID NO:1	TCGAGAATTAAAGGTGAGTGTCTAATGTGAAGTACACCGAGACTGAGATTCAAGTCGG
SEQ ID NO:5	TCGAGAATTAAAGGTGAGTGTCTAATGTGAAGTACACCGAGACTGAGATTCAAGTCGG
SEQ ID NO:9	TCGAGAATTAAAGGTGAGTGTCTAATGTGAAGTACACCGAGACTGAGATTCAAGTCGG
SEQ ID NO:11	TCGAGAATTAAAGGTAGAGAGTCTAATGTGAAGTACACCGAGACTGAGATTCAAGTCGG
SEQ ID NO:13	TCGAGAATTAAAGGTAGAGAGTCTAATGTGAAGTACACCGAGACTGAGATTCAAGTCGG
SEQ ID NO:15	TCGAGAATTAAAGGTAGAGAGTCTAATGTGAAGTACACCGAGACTGAGATTCAAGTCGG
△ △ △	
SEQ ID NO:1	TGTACAAC TACGAA ACC CACCGAAC TTGTT CACGAGAACAGGAATGGCACCTATCAGTGG
SEQ ID NO:5	TGTACAAC TACGAA ACC CACCGAAC TTGTT CACGAGAACAGGAATGGCACCTATCAGTGG
SEQ ID NO:9	TGTACAAC TACGAA ACC CACCGAAC TTGTT CACGAGAACAGGAATGGCACCTATCAGTGG
SEQ ID NO:11	TGTACAAC TACGAA ACC CACCGAAC TTGTT CACGAGAACAGGAATGGCACCTATCAGTGG
SEQ ID NO:13	TGTACAAC TACGAA ACC CACCGAAC TTGTT CACGAGAACAGGAATGGCACCTATCAGTGG
SEQ ID NO:15	TGTACAAC TACGAA ACC CACCGAAC TTGTT CACGAGAACAGGAATGGCACCTATCAGTGG
△ △ △ △ △ △	
SEQ ID NO:1	TTGTCAAACCCAAATCTGTCAAATCGAACATTAAAACCAACATCCATGTTCTAAATTAG
SEQ ID NO:5	TTGTCAAACCCAAATCTGTCAAATCGAACATTAAAACCAACATCCATGTTCTAAATTAG
SEQ ID NO:9	TTGTCAAACCCAAATCTGTCAAATCGAACATTAAAACCAACATCCATGTTCTAAATTAG
SEQ ID NO:11	TTGTCAAACCCAAATCCGTCAACTACCAATTAAAACCAACACCCATGTTCAAATTGG
SEQ ID NO:13	TTGTCAAACCCAAATCCGTCAACTACCAATTAAAACCAACACCCATGTTCAAATTGG
SEQ ID NO:15	TTGTCAAACCCAAATCCGTCAACTACCAATTAAAACCAACACCCATGTTCAAATTGG
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SEQ ID NO:1	GGGTAAATGCTTGTGGGTGGGGTGGAAACAAACGGCTCAACCCTCACCGGTGGTGTATTG
SEQ ID NO:5	GGGTAAATGCTTGTGGGTGGGGTGGAAACAAACGGCTCAACCCTCACCGGTGGTGTATTG
SEQ ID NO:9	GGGTAAATGCTTGTGGGTGGGGTGGAAACAAACGGCTCAACCCTCACCGGTGGTGTATTG
SEQ ID NO:11	GGGTGATGCTTGTGGGTGGGGTGGAAACAAACGGCTCTACCCCTCACCGGTGGTGTATTG
SEQ ID NO:13	GGGTGATGCTTGTGGGTGGGGTGGAAACAAACGGCTCTACCCCTCACCGGTGGTGTATTG
SEQ ID NO:15	GGGTGATGCTTGTGGGTGGGGTGGAAACAAACGGCTCTACCCCTCACCGGTGGTGTATTG

Motif I

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SEQ ID NO:1 CTAACCGAGAGGGCATTCATGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
 SEQ ID NO:5 CTAACCGAGAGGGCATTCATGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
 SEQ ID NO:9 CTAACCGAGAGGGCATTCATGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
 SEQ ID NO:11 CTAACAGAGAGGACATTCATGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG
 SEQ ID NO:13 CTAACAGAGAGGGCATTCATGGCTACAAAGGACAAGATTCAACAAGCCAATTFACTTTG
 SEQ ID NO:15 CTAACAGAGAGGGCATTCATGGCTACAAAGGACAAGATTCAACAAGCCAATTACTTTG

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SEQ ID NO:1 GCTCCCTCACCCAAAGCCTCAGCTATCCGAGTTGGTCCCTCCAGGGAGAGGAATCTATG
 SEQ ID NO:5 GCTCCCTCACCCAAAGCCTCAGCTATCCGAGTTGGTCCCTCCAGGGAGAGGAATCTATG
 SEQ ID NO:9 GCTCCCTCACCCAAAGCCTCAGCTATCCGAGTTGGTCCCTCCAGGGAGAGGAATCTATG
 SEQ ID NO:11 GCTCCCTCACCCAAAGCCTCAGCTATTGAGTTGGATCCTCCAGGGAGAGGAATCTATG
 SEQ ID NO:13 GCTCCCTCACCCAAAGCCTCAGCTATTGAGTTGGATCCTCCAGGGAGAGGAATCTATG
 SEQ ID NO:15 GCTCCCTCACCCAAAGCCTCAGCTATTGAGTTGGATCCTCCAGGGAGAGGAATCTATG

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SEQ ID NO:1 CCCCATTCAAGAGCCTGCTTCAAATGGTTAACCTGACGACATTGTGTTGGGGGATGGG
 SEQ ID NO:5 CCCCATTCAAGAGCCTGCTTCAAATGGTTAACCTGACGACATTGTGTTGGGGGATGGG
 SEQ ID NO:9 CCCCATTCAAGAGCCTGCTTCAAATGGTTAACCTGACGACATTGTGTTGGGGGATGGG
 SEQ ID NO:11 CCCCATTCAAGAGCTGCTTCAAATGGTTAACCTGACGACATTGTGTTGGGGGATGGG
 SEQ ID NO:13 CCCCATTCAAGAGCTGCTTCAAATGGTTAACCTGACGACATTGTGTTGGGGGATGGG
 SEQ ID NO:15 CCCCATTCAAGAGCTGCTTCAAATGGTTAACCTGACGACATTGTGTTGGGGGATGGG

SEQ ID NO:1 ATATCAGCAACATGAACCTGGCTATGCCATGGCCAGGGCAAAGGTGTTGACATCGATT
 SEQ ID NO:5 ATATCAGCAACATGAACCTGGCTATGCCATGGCCAGGGCAAAGGTGTTGACATCGATT
 SEQ ID NO:9 ATATCAGCAACATGAACCTGGCTATGCCATGGCCAGGGCAAAGGTGTTGACATCGATT
 SEQ ID NO:11 ATATCAGCAACATGAACCTGGCTATGCCATGGCCAGGGCAAAGGTGTTGACATCGATT
 SEQ ID NO:13 ATATCAGCAACATGAACCTGGCTATGCCATGGCCAGGGCAAAGGTGTTGACATCGATT
 SEQ ID NO:15 ATATCAGCAACATGAACCTGGCTATGCCATGGCCAGGGCAAAGGTGTTGACATCGATT

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SEQ ID NO:1 TGCAGAACAGCAGTTGAGGCCTTACATGGAATCCATGCTTCACTCCCCGGAATCTATGACC
 SEQ ID NO:5 TGCAGAACAGCAGTTGAGGCCTTACATGGAATCCATGCTTCACTCCCCGGAATCTATGACC
 SEQ ID NO:9 TGCAGAACAGCAGTTGAGGCCTTACATGGAATCCATGCTTCACTCCCCGGAATCTATGACC
 SEQ ID NO:11 TGCAGAACAGCAGTTGAGGCCTTACATGGAATCCATGCTTCACTCCCCGGAATCTACGACC
 SEQ ID NO:13 TGCAGAACAGCAGTTGAGGCCTTACATGGAATCCATGCTTCACTCCCCGGAATCTACGACC
 SEQ ID NO:15 TGCAGAACAGCAGTTGAGGCCTTACATGGAATCCATGCTTCACTCCCCGGAATCTACGACC

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SEQ ID NO:1 CGGATTTCATGCTGCCAACCAAGAGGAGCGTGCCAAACACGTCATCAAGGGCACAAAGC
 SEQ ID NO:5 CGGATTTCATGCTGCCAACCAAGAGGAGCGTGCCAAACACGTCATCAAGGGCACAAAGC
 SEQ ID NO:9 CGGATTTCATGCTGCCAACCAAGAGGAGCGTGCCAAACACGTCATCAAGGGCACAAAGC
 SEQ ID NO:11 CGGATTTCATGCTGCCAACCAAGAGGAGCGTGCCAAACACGTGATTAAGGGCACAAAGC
 SEQ ID NO:13 CGGATTTCATGCTGCCAACCAAGAGGAGCGTGCCAAACACGTGATTAAGGGCACAAAGC
 SEQ ID NO:15 CGGATTTCATGCTGCCAACCAAGAGGAGCGTGCCAAACACGTGATTAAGGGCACAAAGC

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SEQ ID NO:1 AAGAGCAAGTTCAACAAATCATCAAAGACATCAAGGCCTTAAGGAAGCCACCAAAGTGG
 SEQ ID NO:5 AAGAGCAAGTTCAACAAATCATCAAAGACATCAAGGCCTTAAGGAAGCCACCAAAGTGG
 SEQ ID NO:9 AAGAGCAAGTTCAACAAATCATCAAAGACATCAAGGCCTTAAGGAAGCCACCAAAGTGG
 SEQ ID NO:11 AAGAGCAAGTTCAGCAAATCATCAAAGACATCAAGGCCTTAAGGAAGCCACCAAAGTGG
 SEQ ID NO:13 AAGAGCAAGTTCAGCAAATCATCAAAGACATCAAGGCCTTAAGGAAGCCACCAAAGTGG
 SEQ ID NO:15 AAGAGCAAGTTCAGCAAATCATCAAAGACATCAAGGCCTTAAGGAAGCCACCAAAGTGG

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SEQ ID NO:1 ACAAGGTGGTTGACTGTGGACTGCCAACACAGAGAGGTAACAGTAATTGGTTGTGGGCC
 SEQ ID NO:5 ACAAGGTGGTTGACTGTGGACTGCCAACACAGAGAGGTAACAGTAATTGGTTGTGGGCC
 SEQ ID NO:9 ACAAGGTGGTTGACTGTGGACTGCCAACACAGAGAGGTAACAGTAATTGGTTGTGGGCC

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SEQ ID NO:1 ACAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTATAGCAATTGGTTGAGGCC
 SEQ ID NO:13 ACAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTATAGCAATTGGTTGAGGCC
 SEQ ID NO:15 ACAAGGTGGTTGCTGTGGACTGCCAACACAGAGAGGTATAGCAATTGGTTGAGGCC

Motif II

SEQ ID NO:1 TTAATGACACCAGGAGAAATCTCTGGCTGCTGTGGACAGAAATGAGGCTGAGATTCTC
 SEQ ID NO:5 TTAATGACACCAGGAGAAATCTCTGGCTGCTGTGGACAGAAATGAGGCTGAGATTCTC
 SEQ ID NO:9 TTAATGACACCAGGAGAAATCTCTGGCTGCTGTGGACAGAAATGAGGCTGAGATTCTC
 SEQ ID NO:11 TTAATGACACCAGGAGAAATCTCTGGCTGCTGTGGACAGAAATGAGGCTGAGATTCTC
 SEQ ID NO:13 TTAATGACACCAGGAGAAATCTCTGGCTGCTGTGGACAGAAATGAGGCTGAGATTCTC
 SEQ ID NO:15 TTAATGACACCAGGAGAAATCTCTGGCTGCTGTGGACAGAAATGAGGCTGAGATTCTC

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SEQ ID NO:1 CTTCCACCTTGATGCCATTGCTGTGTTATGGAAAATGTTCCCTTCATTAATGGAAGCC
 SEQ ID NO:5 CTTCCACCTTGATGCCATTGCTGTGTTATGGAAAATGTTCCCTTCATTAATGGAAGCC
 SEQ ID NO:9 CTTCCACCTTGATGCCATTGCTGTGTTATGGAAAATGTTCCCTTCATTAATGGAAGCC
 SEQ ID NO:11 CTTCCACCTTGATGCCATTGCTGTGATGGAAAATGTTCCCTTCATTAATGGAAGCC
 SEQ ID NO:13 CTTCCACCTTGATGCCATTGCTGTGATGGAAAATGTTCCCTTCATTAATGGAAGCC
 SEQ ID NO:15 CTTCCACCTTGATGCCATTGCTGTGATGGAAAATGTTCCCTTCATTAATGGAAGCC

SEQ ID NO:1 CTCAGAACACTTTGTACCAGGGCTGATTGATCTGCCATCGCGAGGAACACTTGTATTG
 SEQ ID NO:5 CTCAGAACACTTTGTACCAGGGCTGATTGATCTGCCATCGCGAGGAACACTTGTATTG
 SEQ ID NO:9 CTCAGAACACTTTGTACCAGGGCTGATTGATCTGCCATCGCGAGGAACACTTGTATTG
 SEQ ID NO:11 CTCAGAACACTTTGTACCAGGGCTGATTGATCTGCCATCGCGAGGAACACTTGTATTG
 SEQ ID NO:13 CTCAGAACACTTTGTACCAGGGCTGATTGATCTGCCATCGCGAGGAACACTTGTATTG
 SEQ ID NO:15 CTCAGAACACTTTGTACCAGGGCTGATTGATCTGCCATCGCGAGGAACACTTGTATTG

Motif III

SEQ ID NO:1 GTGGAGATGACTTCAAGAGTGGTCAGACCAAAATGAAATCTGTGTGGTTGATTCCCTTG
 SEQ ID NO:5 GTGGAGATGACTTCAAGAGTGGTCAGACCAAAATGAAATCTGTGTGGTTGATTCCCTTG
 SEQ ID NO:9 GTGGAGATGACTTCAAGAGTGGTCAGACCAAAATGAAATCTGTGTGGTTGATTCCCTTG
 SEQ ID NO:11 GTGGAGATGACTTCAAGAGTGGTCAGACCAAAATGAAATCTGTGTGGTTGATTCCCTTG
 SEQ ID NO:13 GTGGAGATGACTTCAAGAGTGGTCAGACCAAAATGAAATCTGTGTGGTTGATTCCCTTG
 SEQ ID NO:15 GTGGAGATGACTTCAAGAGTGGTCAGACCAAAATGAAATCTGTGTGGTTGATTCCCTTG

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SEQ ID NO:1 TGGGGGCTGGTATCAAGCCAACATCTATAGTCAGTTACAACCATCTGGAAACATGATG
 SEQ ID NO:5 TGGGGGCTGGTATCAAGCCAACATCTATAGTCAGTTACAACCATCTGGAAACATGATG
 SEQ ID NO:9 TGGGGGCTGGTATCAAGCCAACATCTATAGTCAGTTACAACCATCTGGAAACATGATG
 SEQ ID NO:11 TGGGGGCTGGTATCAAGCCAACATCTATAGTTAGTTACAACCATCTGGAAACATGATG
 SEQ ID NO:13 TGGGGGCTGGTATCAAGCCAACATCTATAGTTAGTTACAACCATCTGGAAACATGATG
 SEQ ID NO:15 TGGGGGCTGGTATCAAGCCAACATCTATAGTTAGTTACAACCATCTGGAAACATGATG

Motif IV

SEQ ID NO:1 GTATGAATCTTCGGCTCCACAAACATTCCGGTCCAAGGAAATCTCCAAGAGCAACGTTG
 SEQ ID NO:5 GTATGAATCTTCGGCTCCACAAACATTCCGGTCCAAGGAAATCTCCAAGAGCAACGTTG
 SEQ ID NO:9 GTATGAATCTTCGGCTCCACAAACATTCCGGTCCAAGGAAATCTCCAAGAGCAACGTTG
 SEQ ID NO:11 GTATGAATCTCTCGGCTCCACAAACCTCCGGTCCAAGGAAATCTCCAAGAGCAACGTTG
 SEQ ID NO:13 GTATGAATCTCTCGGCTCCACAAACCTCCGGTCCAAGGAAATCTCCAAGAGCAACGTTG
 SEQ ID NO:15 GTATGAATCTCTCGGCTCCACAAACCTCCGGTCCAAGGAAATCTCCAAGAGCAACGTTG

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SEQ ID NO:1 TTGATGATATGGTCAACAGCAATGCCATCCTATGAGCCTGGTGAACATCCAGACCATG
 SEQ ID NO:5 TTGATGATATGGTCAACAGCAATGCCATCCTATGAGCCTGGTGAACATCCAGACCATG
 SEQ ID NO:9 TTGATGATATGGTCAACAGCAATGCCATCCTATGAGCCTGGTGAACATCCAGACCATG
 SEQ ID NO:11 TTGACGATATGGTCAACAGCAATGCCATCCTATGAGCCTGGTGAACATCCAGACCATG
 SEQ ID NO:13 TTGACGATATGGTCAACAGCAATGCCATCCTATGAGCCTGGTGAACATCCAGACCATG
 SEQ ID NO:15 TTGACGATATGGTCAACAGCAATGCCATCCTATGAGCCTGGTGAACATCCAGACCATG

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SEQ ID NO:1 TTGTTGTTATTAAGTATGTGCCTTACGTAGGGACAGCAAGAGAGCCATGGATGAGTACA
 SEQ ID NO:5 TTGTTGTTATTAAGTATGTGCCTTACGTAGGGACAGCAATAGAGCCATGGATGAGTACA
 SEQ ID NO:9 TTGTTGTTATTAAGTATGTGCCTTACGTAGGGACACCAAGAGAGCCATGGATGAGTACA
 SEQ ID NO:11 TTGTTGTTATTAAGTATGTGCCTTACGTAGGGATAGCAAGAGAGCCATGGATGAGTACA
 SEQ ID NO:13 TTGTTGTTATTAAGTATGTGCCTTACGTAGGGATAGCAAGAGAGCCATGGATGAGTACA
 SEQ ID NO:15 TTGTTGTTATTAAGTATGTGCCTTACGTAGGGATAGCAAGAGAGCCATGGATGAGTACA

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SEQ ID NO:1 CTTCAGAGATATTCTGGGTGGAAAGAGCACCATTGTTTGACACAACACATGCGAGGATT
 SEQ ID NO:5 CTTCAGAGATATTCTGGGTGGAAAGAGCACCATTGTTTGACACAACACATGCGAGGATT
 SEQ ID NO:9 CTTCAGAGATATTCTGGGTGGAAAGAGCACCATTGTTTGACACAACACATGCGAGGATT
 SEQ ID NO:11 CTTCAGAGATATTCTGGGTGGAAAGAACACCATTGTTTGACACAACACATGCGAGGATT
 SEQ ID NO:13 CTTCAGAGATATTCTGGGTGGAAAGAACACCATTGTTTGACACAACACATGCGAGGATT
 SEQ ID NO:15 CTTCAGAGATATTCTGGGTGGAAAGAACACCATTGTTTGACACAACACATGCGAGGATT

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SEQ ID NO:1 CCCTCTTAGCTGCTCTATTATCTTGGACTTGGCCTCTTGCTGAGCTCAGCACTAGAA
 SEQ ID NO:5 CCCTCTTAGCTGCTCTATTATCTTGGACTTGGCCTCTTGCTGAGCTCAGCACTAGAA
 SEQ ID NO:9 CCCTCTTAGCTGCTCTATTATCTTGGACTTGGCCTCTTGCTGAGCTCAGCACTAGAA
 SEQ ID NO:11 CCCTCTTAGCTGCTCTATTATCTTGGACTTGGCCTCTTGCTGAGCTGAGCACTAGAA
 SEQ ID NO:13 CCCTCTTAGCTGCTCTATTATCTTGGACTTGGCCTCTTGCTGAGCTGAGCACTAGAA
 SEQ ID NO:15 CCCTCTTAGCTGCTCTATTATCTTGGACTTGGCCTCTTGCTGAGCTGAGCACTAGAA

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SEQ ID NO:1 TCGAGTTAAAGCTGAAAATGAGGGAAAATTCCACTCATTCACCCAGTTGCTACCATTC
 SEQ ID NO:5 TCGAGTTAAAGCTGAAAATGAGGGAAAATTCCACTCATTCACCCAGTTGCTACCATTC
 SEQ ID NO:9 TCGAGTTAAAGCTGAAAATGAGGGAAAATTCCACTCATTCACCCAGTTGCTACCATTC
 SEQ ID NO:11 TCCAGTTAAAGCTGAAAATGAGGGAAAATTCCACTCATTCACCCAGTTGCTACCATTC
 SEQ ID NO:13 TCCAGTTAAAGCTGAAAATGAGGGAAAATTCCACTCATTCACCCAGTTGCTACCATTC
 SEQ ID NO:15 TCCAGTTAAAGCTGAAAATGAGGGAAAATTCCACTCATTCACCCAGTTGCTACCATTC

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SEQ ID NO:1 TCAGCTACCTCACCAAGGCTCCTCTGGTTCACCCAGTTGCTACCATTC
 SEQ ID NO:5 TCAGCTACCTCACCAAGGCTCCTCTGGTTCACCCAGTTGCTACCATTC
 SEQ ID NO:9 TCAGCTACCTCACCAAGGCTCCTCTGGTTCACCCAGTTGCTACCATTC
 SEQ ID NO:11 TCAGCTATCTGACCAAGGCTCCTCTGGTTCACCCAGTTGCTACCATTC
 SEQ ID NO:13 TCAGCTATCTGACCAAGGCTCCTCTGGTTCACCCAGTTGCTACCATTC
 SEQ ID NO:15 TCAGCTATCTGACCAAGGCTCCTCTGGTTCACCCAGTTGCTACCATTC

SEQ ID NO:1 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
 SEQ ID NO:5 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
 SEQ ID NO:9 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
 SEQ ID NO:11 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
 SEQ ID NO:13 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA
 SEQ ID NO:15 CAAAGCAGCGTGCAATGCTGGAAAACATAATGAGGGCTTGTGTTGGATTGGCCCCAGAGA

SEQ ID NO:1 ATAACATGATTCTCGAGTACAAGTGAAGCATGGACCGAAGAATAATAGTTGGGTAG
 SEQ ID NO:5 ATAACATGATTCTCGAGTACAAGTGA-----
 SEQ ID NO:9 ATAACATGATTCTCGAGTACAAGTGA-----
 SEQ ID NO:11 ATAACATGATTCTCGAGTACAAGTGA-----
 SEQ ID NO:13 ATAACATGATTCTCGAGTACAAGTGA-----
 SEQ ID NO:15 ATAACATGATTCTCGAGTACAAGTGA-----

SEQ ID NO:1 CCTAGCTGAATGTTTATGTTAATAATATGTTGCTTATAATTGCAAGTGTATTGAA
 SEQ ID NO:5 -----
 SEQ ID NO:9 -----
 SEQ ID NO:11 -----
 SEQ ID NO:13 -----
 SEQ ID NO:15 -----

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SEQ ID NO:1 TGCATCAGCTTCATTAATGCTTAGAGCGGGCATATTCTGTTACTAGGAACATGAATG
SEQ ID NO:5 -----
SEQ ID NO:9 -----
SEQ ID NO:11 -----
SEQ ID NO:13 -----
SEQ ID NO:15 -----

SEQ ID NO:1 AATGTAGTATAATTTGTGT
SEQ ID NO:5 -----
SEQ ID NO:9 -----
SEQ ID NO:11 -----
SEQ ID NO:13 -----
SEQ ID NO:15 -----

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